CLAIMS

[1] A method of assaying whether a chemical is present in a test specimen or not, comprising culturing a gene-disrupted strain of a microorganism in the presence of the test specimen, and using cell response of the gene-disrupted strain to the chemical as an index.

[2] The method according to claim 1, wherein the cell response of a gene-disrupted strain to a chemical is life or death of a cell, and/or proliferation ability, aspiration amount, enzyme activity and/or a change in gene expression.

[3] The method according to claim 2, wherein the change in gene expression is a change in a RNA amount or a mRNA amount.

[4] The method according to claim 2, wherein the change in gene expression is measured by reporter·gene·assay.

[5] The method according to any one of claims 1 to 4, wherein the microorganism is yeast.

[6] The method according to claim 5, wherein a gene to be

disrupted is classified into:

amino acid metabolism (01.01), nitrogen and sulfur metabolism (01.02), nucleotide metabolism (01.03), phosphate metabolism (01.04), C-compound and carbohydrate metabolism (01.05), lipid, fatty acid and isoprenoid metabolism (01.06), metabolism of vitamins, cofactors and prosthetic groups (01.07) of metabolism (01);

DNA processing (03.01), cell cycle (03.03) of cell cycle and DNA processing (03);

mRNA transcription (04.05), RNA transport (04.07) of transcription (04);

ribosome biosynthesis (05.01), translation control (05.07) of protein synthesis (05);

protein targeting, sorting, translocation (06.04), protein modification (06.07), assembly of protein complex (06.10), proteolysis (06.13) of protein fate (06);

nuclear transport (08.01), vesicular transport (Golgi network etc) (08.07), vacuolar transport (08.13), cellular import (08.19), cytoskeleton-dependent transport (08.22), other intracellular transport activities (08.99) of intracellular transport and transport mechanism (08);

stress response (11.01), detoxification (11.07) of cell rescue, defense and pathogemicity (11);

ionic homeostasis (13.01), cell sensitivity and response (13.11) of intracellular environmental

regulation/interaction (13);

cell growth/morphogenesis (14.01), cell differentiation (14.04) of cell fate (14);

cell wall (30.01), cytoskeleton (30.04), nucleus (30.10), mitochondria (30.16) of cell tissue control (30);

ion transporter (67.04), vitamin/cofactor transporter (67.21), transport mechanism (67.50), other transport promotion (67.99) of transport promotion (67);

unclassified (98); and/or

unclassified protein (99).

[7] The method according to claims 6, wherein the gene to be disrupted is involved in a vacuole.

[8] The method according to claim 6, wherein the metabolism (01) gene to be disrupted is YGL026C, YGR180C, YDR127W, YCR028C, YLR284C, YOR221C, YAL021C, YGL224C, YBL042C, YDR148C, YHL025W, YLR307W, YLR345W, YLR354C, YPL129W, or YPR060C.

[9] The method according to claim 6, wherein the cell cycle and DNA processing (03) gene to be disrupted is YGR180C, YDR150W, YGL240W, YBL058W, YIL036W, YLR226W, YLR381W, YOR026W, YPL018W, YBL063W, YDR363W-A, YIR026C, YLR234W, YMR032W or YPL129W.

[10] The method according to claim 6, wherein the transcription (04) gene to be disrupted is YGR006W, YIL036W, YKR082W, YLR226W, YML112W, YMR021C, YAL021C, YDR195W, YOL068C, YBR279W, YGL070C, YGL071W, YGL222C, YHL025W, YLR266C or YPL129W.

[11] The method according to claim 6, wherein the protein synthesis (05) gene to be disrupted is YBL058W, YLR287C-A, YGR084C or YLR344W.

[12] The method according to claim 6, wherein the protein fate (06) gene to be disrupted is YKL080W, YLR447C, YGL240W, YGR105W, YGL206C, YKL119C, YDR414C, YHR060W, YLR292C, YLR306W, YGL227W or YGR270W.

[13] The method according to claim 6, wherein the intracellular transport and transport mechanism (08) gene to be disrupted is YPR036W, YDR027C, YHR039C, YKL080W, YLR447C, YGL206C, YKR082W, YLR292C or YBL063W.

[14] The method according to claim 6, wherein the detoxification (11) gene to be disrupted is YJR104C or YMR021C.

[15] The method according to claim 6, wherein the intracellular regulation/interaction (13) gene to be disrupted is YPR036W, YHR039C-B, YKL080W, YLR447C, YGL071W or YIR026C.

[16] The method according to claim 6, wherein the cell fate (14) gene to be disrupted is YDL151C, YBL058W, YKR082W, YDL151C, YOL068C, YDR363W-A, YHL025W, YIR026C, YLR307W, YMR032W or YPL129W.

[17] The method according to claim 6, wherein the cell tissue control (30) gene to be disrupted is YDR027C, YDR414C, YLR381W, YGR084C or YMR032W.

[18] The method according to claim 6, wherein the transport promotion (67) gene to be disrupted is YPR036W, YHR026W, YHR039C, YKL080W, YLR447C, YCR028C or YLR292C.

[19] The method according to claim 6, wherein the unclassified (98) gene to be disrupted is YBL056W.

[20] The method according to claim 6, wherein the unclassified protein (99) gene to be disrupted is YDR149C, YLR285W, YLR311C, YOR331C, YPR123C, YDR525W-A, YDR539W, YDR540C, YGL246C, YJL204C, YLR282C, YLR287C, YLR290C,

YJL188C, YJL192C, YJL211C, YKL037W, YLR283W, YLR312C, YLR315W, YLR320W or YPL030W.

[21] A kit containing a gene-disrupted strain of a microorganism, which is used for detecting whether a chemical is present in a test specimen or not.

[22] A composition containing a gene-disrupted strain of a microorganism, for detecting whether a chemical is present in a test specimen or not.

[23] Use of a gene-disrupted strain of a microorganism, for detecting whether a chemical is present in a test specimen or not.